

cDNA Sequence of human IBR

Two alternative 5' ends:

1	TTGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAA
2	AAGGAAGGAGGGAGAAGGGAAGGAGTGAAGGAAGGAGTGAAA

Common Sequence:

<u>AGGGGAGTCTACACCCTGTGGAGCTCAAGATGGTCCTGAGTGGGGCGCTGTGCTTCCGAA</u>		60
<u>TGAAGGACTCGGCATTGAAGGTGCTTTATCTGCATAATAACCAGCTTCTAGCTGGAGGGC</u>		120
<u>TGCATGCAGGGAAGGTCATTAAAGGTGAAGAGATCAGCGTGGTCCCCAATCGGTGGCTGG</u>		180
<u>ATGCCAGCCTGTCCCCCGTCATCCTGGGTGTCCAGGGTGGAAGCCAGTGCCTGTCATGTG</u>		240
<u>GGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG</u>		300
<u>GTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGGCGGGACATGGGGCTCACCTCCAGCT</u>		360
<u>TCGAGTCGGCTGCCTACCCGGGCTGGTTTCTGTGCACGGTGCCTGAAGCCGATCAGCCTG</u>		420
<u>TCAGACTCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCCATCACAGACTTCTACT</u>		480
<u>TCCAGCAGTGTGACTAGGGCAACGTGCCCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGG</u>		540
<u>GTGAGGGGTGAGTGGAGGAGACCCATGGCGGACAATCACTCTTCTGCTCTCAGGACCCC</u>		600
<u>CAGGTCTGACTTAGTGGGCACCTGACCACTTTGTCTTCTGGTTCCAGTTTGCATAAATT</u>		660
<u>CTGAGATTTGGAGCTCAGTCCAGGGTCCTCCCCCACTGGATGGTGCTACTGCTGTGGAAC</u>		720
<u>CTTGTA AAAACCATGTGGGGTAAACTGGGAATAACATGAAAAGATTTCTGTGGGGGTGGG</u>		780
<u>GTGGGGGAGTGCTGGGAATCATTCCTGCTTAATGGTAACTGACAAGTGTTACCCTGAGCC</u>		840
<u>CCGCAGGCCAACC CATCCCCAGTTGAGCCTTATAGGGTCAGTAGCTCTCCACATGAAGTC</u>		900
<u>CTCTCACTCACC ACTGTGCAGGAGAGGGAGGTGGTCATAGAGTCAGGGATCTATGGCCCT</u>		960
<u>TGGCCCAGCCCCACCCCTTCCCTTTATCCTGCCACTGTCATATGCTACCTTTCCTATCT</u>		1020
<u>CTTCCCTCATCATCTTGTTGTGGGCATGAGGAGGTGGTGATGTCAGAAGAAATGGTTCGA</u>		1080
<u>GCTCAGAAGATAAAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCAAGATACAA</u>		1140
<u>TCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAAGTGCTCATGACATATTGAGAAG</u>		1200
<u>ACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAAATTAAGATACTATTTATAT</u>		1260
<u>ATTTCTTTATAGAAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTCAGGGTGGT</u>		1320
<u>GGCAGTATAGGTGATTTTTCTTTTAAATTCTGTTAATTTATCTGTATTTCTTAATTTTCT</u>		1380
<u>ACAATGAAGATGAATTCCTTGTATAAAAATAAGAAAAGAAATTAATCTTGAGGTAAGCAG</u>		1440

FIG. 1

DATE	DESCRIPTION	AMOUNT	BALANCE
1/1/01	OPENING BALANCE		100.00
1/15/01	PAYROLL	10.00	90.00
1/20/01	RENT	20.00	70.00
1/25/01	SALES	50.00	120.00
1/30/01	PAYROLL	10.00	110.00
2/5/01	RENT	20.00	90.00
2/10/01	SALES	60.00	150.00
2/15/01	PAYROLL	10.00	140.00
2/20/01	RENT	20.00	120.00
2/25/01	SALES	70.00	190.00
2/28/01	PAYROLL	10.00	180.00
3/5/01	RENT	20.00	160.00
3/10/01	SALES	80.00	240.00
3/15/01	PAYROLL	10.00	230.00
3/20/01	RENT	20.00	210.00
3/25/01	SALES	90.00	300.00
3/30/01	PAYROLL	10.00	290.00
3/31/01	CLOSING BALANCE		290.00

AGCAGACATCATCTCTGATTGTCTCAGCCTCCAATTCCCCAGAGTAAATTCAAATTGAA	1500
TCGAGCTCTGCTGCTCTGGTTGGTTGTAGTAGTGATCAGGAAACAGATCTCAGCAAAGCC	1560
ACTGAGGAGGAGGCTGTGCTGAGTTTGTGTGGCTGGAATCTCTGGGTAAGGAAGTTAAAG	1620
AACAAAAATCATCTGGTAATTCTTTCCTAGAAGGATCACAGCCCCTGGGATTCCAAGGCA	1680
TTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGAATTGTGTCCCCCTCAAATTCAC	1740
ATCCTTCTTGGAAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGCAGATGTAGT	1800
TAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTAAATTC AATATGACTGGTTTCCT	1860
TGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTAAAGATGA	1920
AGGCAGAGATCGGAGTTTTTGCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACCAT	1980
CAGAAGCTTGGAAGAGGCAAAGAAGAATTCTTCCCTAGAGGCTTTAGAGGGATAACGGCT	2040
CTGCTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAACGAAGAAAGAATAAATTTCGGC	2100
TGTTTTTAAGCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAACTAATACAGCTGCTA	2160
AAATGATCCCTGTCTCCTCGTGTTTACATTCTGTGTGTGTCCCCCTCCACAATGTACCAA	2220
AGTTGTCTTTGTGACCCAATAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATTA	2280
GGTTATAAAAGACACTGCAGCTTCTACTTGAGCCCTCTCTCTCTGCCACCCACCGCCCCC	2340
AATCTATCTTGGCTCACTCGCTCTGGGGGAAGCTAGCTGCCATGCTATGAGCAGGCCTAT	2400
AAAGAGACTTACGTGGTAAAAAATGAAGTCTCCTGCCCACAGCCACATTAGTGAACCTAG	2460
AAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTGTTTTAAGTTGCTCAGTTTTGGTCTA	2520
ACTTGTTATGCAGCAATAGATAAATAATATGCAGAGAAAGAG (A _n)	2562

cDNA Sequence of murine IBR

GGCACGAGGGGAGCCTGCTTTCTACTTAGGTCTCAAATTTTCCAGCCTTGTCTTTGCCTA 60
AAATTTCTGCTGTTTATTTCAAATAGGGTCTACATACTGTGGAGCTCATGATGGTTCT 120
GAGTGGGGCACTATGCTTCCGAATGAAGGATTGAGCCTTGAAGGTACTGTATCTGCACAA 180
TAACCAGCTGCTGGCTGGAGGACTGCACGCAGAGAAGGTCATTAAAGGTGAGGAGATCAG 240
TGTTGTCCCAAATCGGGCACTGGATGCCAGTCTGTCCCCTGTCATCCTGGGCGTTCAAGG 300
AGGAAGCCAGTGCCTATCTTGTGGGACAGAGAAAGGGCCAATTCTGAAACTTGAGCCAGT 360
GAACATCATGGAGCTCTACCTCGGGGCCAAGGAATCAAAGAGCTTCACCTTCTACCGGCG 420
GGATATGGGTCTTACCTCCAGCTTCGAATCCGCTGCCTACCCAGGCTGGTTTCTCTGCAC 480
CTCACCGGAAGCTGACCAGCCTGTGAGGCTCACTCAGATCCCTGAGGACCCCGCCTGGGA 540
TGCTCCCATCACAGACTTCTACTTTCAGCAGTGTGACTAGGGCTGCGTGGTCCCCAAAAC 600
TCCATAAGCAGAGGCAGAGTAGGCAGTGGCGGCTCCTGATAGAGGATAGAGAGACAGAGG 660
AGCTCCACAGTAGGTGGCTTACTCCTCTCCTTCCCTACTGGACTCCCGCTTCTGACCTAA 720
GGCACACAGACACTCTCTTCTCCTGCATCCCAGTGCTGGTAAATCTTCTGGTATTTGGAG 780
CTCAATGTGTAGATTCTTTCAGATTGGATGGTACTACCTCTGGTGTGGAACCCAATAGAA 840
ACCACGTAGGACCAACAAAGAGCAACATAAAAGATTCTTGGGTGAAGAAGAGGTGGGAAC 900
TGTTTCATACATAGTAAGATCTGACACAGTACCTCAGAAGTCCTGCCATTCCCTTATGTTCT 960
GGAGAAAGTGGAGGGGGGGTCCACCAAGACTTTCTCTGGCTGGCTGGGCCCTTTCCCTCAA 1020
CCTTTCTGACATCTGCAGCCTCTCTCATTCTTGCCTTCATTCTCTGGCCCTGAACCGAGA 1080
GGGTGATATCAGGATAGCTGACAGAAGATGACCAGGCACACTGTCCTGGTTTGAAACCAG 1140
AGGGGACAATAAAAAACCTGATTCTGGTCTCTACTCACATAAAAAGAAGCTTGTGAACA 1200
TTAAGTGGGAAGAGATTGCTACTAAATAACATACCTTGTAATTTTCATCTTAATTAATA 1260
TACTTCTCTATATTATATATTTTA_(n) 1284

FIG. 2

IBR Polypeptides

(A) Human IBR polypeptide

MVLSGALCFR MKDSALKVLY LHNNQLLAGG LHAGKVIKGE EISVVPNRWL
DASLSPVILG VQGSQCLSC GVGQEPTLTL EPVNIMELYL GAKESKSFTF
YRRDMGLTSS FESAAYPGWF LCTVPEADQP VRLTQLPENG GWNAPITDFY
FQQCD

(B) Mouse IBR polypeptide

MVLSGALCFR MKDSALKVLY LHNNQLLAGG LHAEKVIKGE EISVVPNRAL
DASLSPVILG VQGSQCLSC GTEKGPIILKL EPVNIMELYL GAKESKSFTF
YRRDMGLTSS FESAAYPGWF LCTSPEADQP VRLTQIPEDP AWDAPITDFY
FQQCD

FIG. 3

Comparison of Human and Mouse IBR Polypeptide Sequences

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mIBR: 1  MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAEKVIKGEESVVPNRALDASLSPVILG 60
          MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHA KVIKGEESVVPNR-LDASLSPVILG IBRcon.
hIBR: 1  MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEESVVPNRWLDASLSPVILG 60

mIBR: 61  VQGSQCLSCGTEKGPIKLPEVNMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWF 120
          VQGSQCLSCG--+-P+L-LEPVNMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWF IBRcon.
hIBR: 61  VQGSQCLSCGVGQEPTLTLEPVNMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWF 120

mIBR: 121 LCTSPEADQPVRILTQIPEDPAWDAPITDFYFQQCD 155
          LCT-PEADQPVRILTQ+PE+--W+APITDFYFQQCD IBRcon.
hIBR: 121 LCTVPEADQPVRILTQLPENGWGNAPITDFYFQQCD 155
  
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FIG. 4

00617720-074700

Comparison of Human IBR and pro-IL-1ra Polypeptide Sequences

hIL-1ra:	38	FRIWDVNQKTFYLRNNQLVAGYLQGPVNVNLEEKIDVVP-----IEPHALFLGIHGGKM	90
		FR+ D K YL NNQL+AG L V E+I VVP + P + LG+ GG	con.
hIBR	: 9	FRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEESISVVPNRWLDASLSP--VILGVQGSQ	66
hIL-1ra:	91	CLSCVKSGDETRLQLEAVNITDLSNRKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAM	150
		CLSC G E L LE VNI +L K+ K F F R D G T+SFESAA PGWFLCT	con.
hIBR	: 67	CLSC-GVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVP	125
hIL-1ra:	151	EADQPVSLTNMPDEG---VMVTKFYFQE	175
		EADQPV LT +P+ G +T FYFQ+	con.
hIBR	: 126	EADQPVRLTQLPENGGWNAPITDFYFQQ	153

FIG. 5

002227500

Recombinant IBR Polypeptides

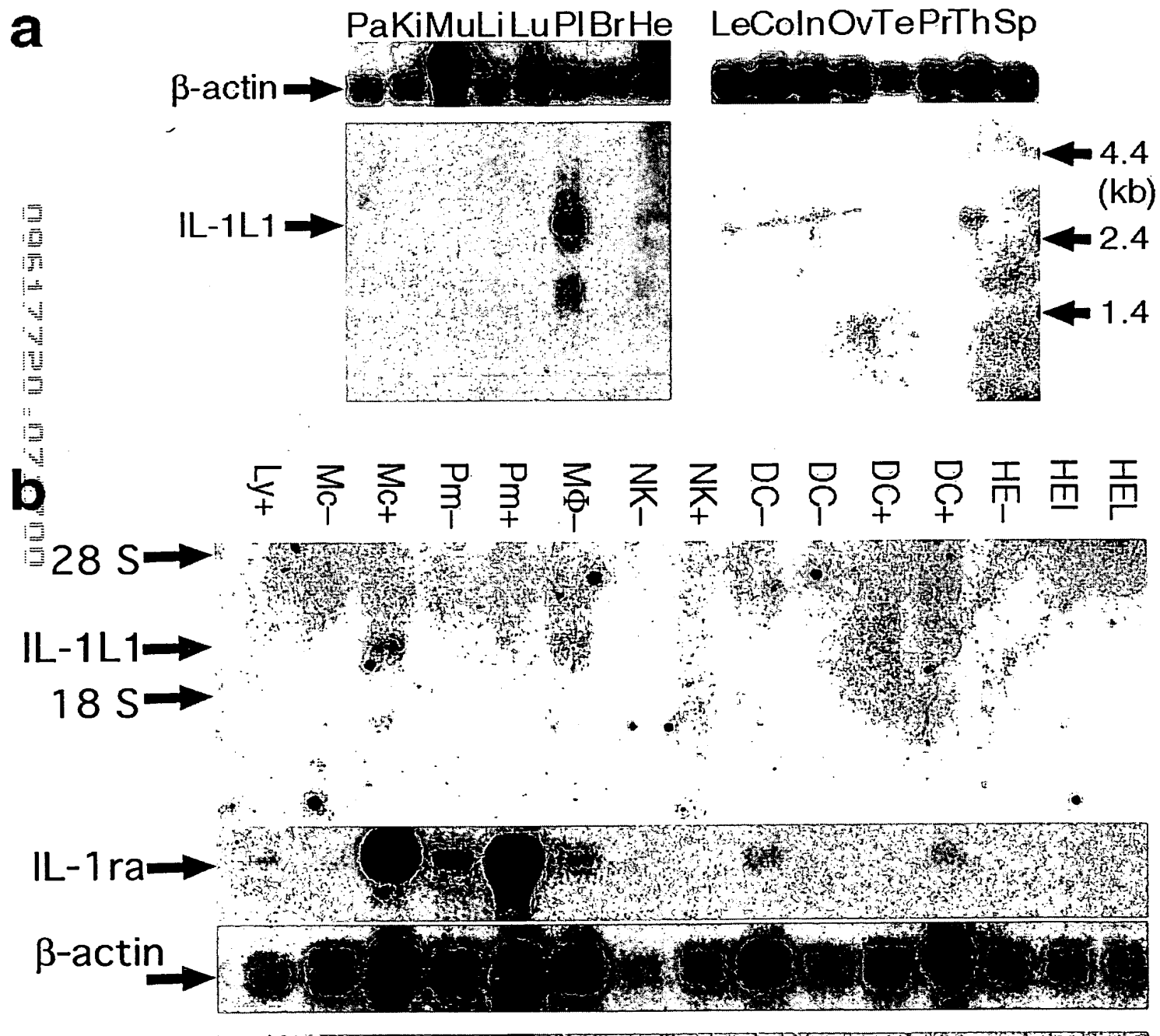
MVLSGALCFR MKDSALKVLY LHNNQLLAGG LHAGKVIKGE EISVVPNRWL
DASLSPVILG VQGGSQCLSC GVGQEPTLTL EPVNIMELYL GAKESKSFTF
YRRDMGLTSS FESAAYPGWF LCTVPEADQP VRLTQLPENG GWNAPITDFY
FQQCD

VLSGALCFR MKDSALKVLY LHNNQLLAGG LHAGKVIKGE EISVVPNRWL
DASLSPVILG VQGGSQCLSC GVGQEPTLTL EPVNIMELYL GAKESKSFTF
YRRDMGLTSS FESAAYPGWF LCTVPEADQP VRLTQLPENG GWNAPITDFY
FQQCD

GSSVLSGALCFR MKDSALKVLY LHNNQLLAGG LHAGKVIKGE EISVVPNRWL
DASLSPVILG VQGGSQCLSC GVGQEPTLTL EPVNIMELYL GAKESKSFTF
YRRDMGLTSS FESAAYPGWF LCTVPEADQP VRLTQLPENG GWNAPITDFY
FQQCD

FIG. 6

FIG. 7



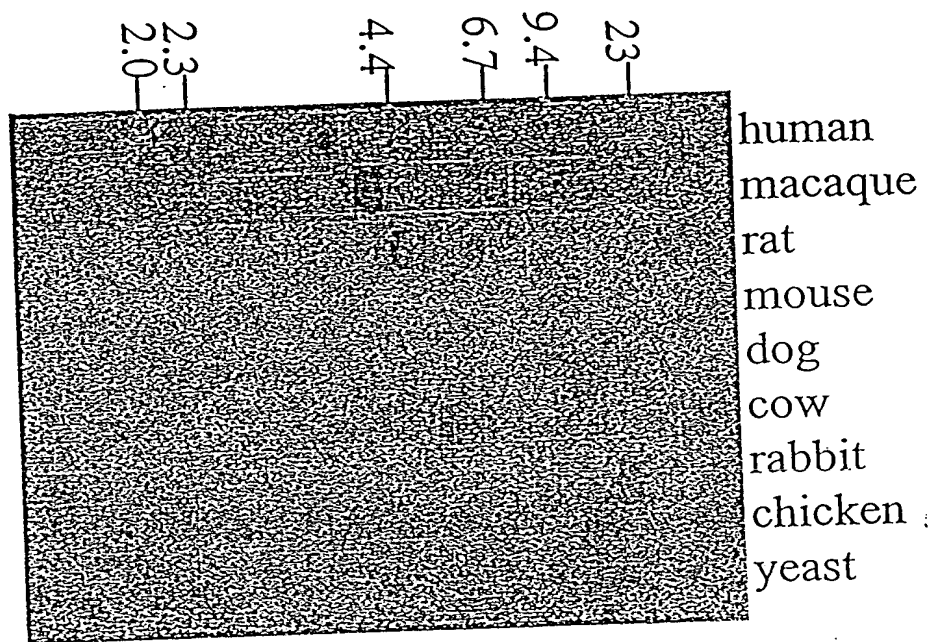
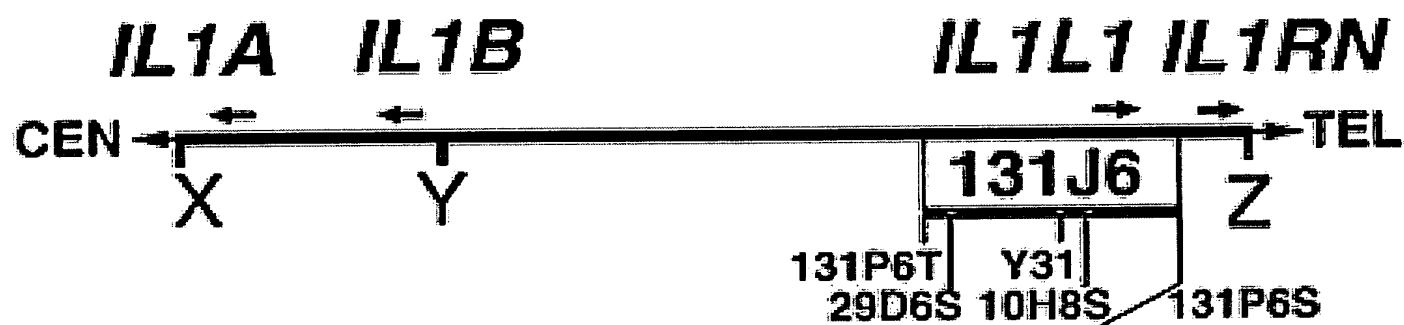
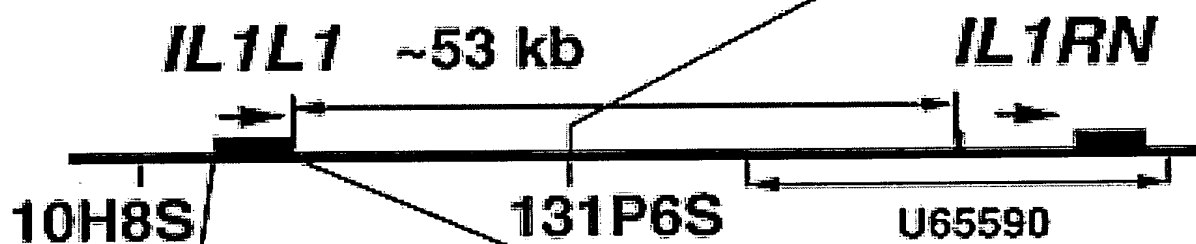


FIG. 8

a



b



c

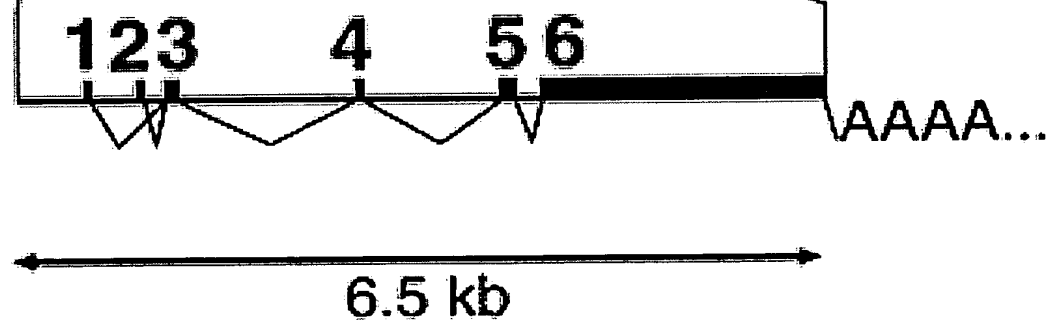


FIG. 9

a

cDNA SEQUENCES CONTAINING EXON 1

CTGGCAATGGCAGGCAGGAAAGACAGAGGAAGGAAGGAGGGAGAAGGGAAGGAGTGAAGGAAGGAGTGAAAAA// exon 3

^
-74' M A G R K D R G R K E G E G K E ***

cDNA SEQUENCES CONTAINING EXON 2

TTGGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAAAGGAACATTCTGAG// exon 3

^
-54

b

5' flank	start exon	start seq	cDNA	end seq	end	3' flank
	+ 451	1	CTGGCAATGG	-74' -	-1'	AGTGAAAAAG + 524 gtaaggaaga
	+ 969	2	TTGGAGGAAC	-54 -	-1	ACATTCTGAG +1022 gtatgctctg
tccaaaatag	+1193	3	GGGAGTCTAC	1 -	56	TGTGCTTCCG +1248 gtgagtgtat
gatgtttcag	+2631	4	AATGAAGGAC	57 -	142	GTCATTAAAG +2716 gttggtgatg
tttcccacag	+3905	5	GTGAAGAGAT	143 -	270	AACACTAGAG +4032 gtgagacttg
ctgccggcag	+4234	6	CCAGTGAACA	271 -	2559	AGAGAAAGAG +6522 aaacaaatgc

c

IL-1L1 MVLSGALCFR⁽²⁾MKDSALKVLYLHNNQLLAGGLHAGKVIKG⁽¹⁾EEISVVPNRWLDASLSP
IL-1ra ..RKSSKMQAFR⁽²⁾IWDVNQKTFYLRNNQLVAGYLQGPVNLEE⁽¹⁾KIDVVP-----IEPHA

IL-1L1 VILGVQGGSQCLSCG-VGQEPTLTLE⁽³⁾VNIMELYLGAKESKSFTFYRRDM..
IL-1ra LFLGIHGGKMCLSCVKSGDETRLQLE⁽³⁾VNITDLSNRKQDKRFAFIRSDS..

FIG. 10

[illegible]

1/6

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1  CATGAGCAAA  GATGTTAATA  CAAAGATGTT  TGTCAACAAC  TGGTTTTCAA  TAGCAAAAAA

61  AGAGAGAAAA  ATATATAAAA  GACAAATAAC  AGTGGATAGG  TTTCAATAAA  TAATGTTACA

121  GTGATACAGT  TAAATACTAT  ACAGCTATTG  AAGCATGTCA  TTATTCATAT  TTAGTATGGA

181  AAGATATTTT  GCTATTTTGC  TACATGAAAA  AATGAGGTTG  GAAAAAGTAT  AGGTTTTGTG

241  AATCTGTTGT  ATGAAAGCTG  TCTATAGTTA  CATGTGTATG  TGTGTGGAGG  AAAAAGTGTT

301  GTCATTGGTT  TTCTGATGAT  GCACTCAGAA  AAGACAAGTA  TTCACATTTT  TTCTTGTTGC

361  TGATCTGGAT  TTTCAGGTTT  TTCTACAATG  AACATGTAGG  CTGAACATTC  CCTAAGCAGG

421  AGAGTCCCAC  CTCTAACATC  TCCTGTAGGC  CTGGCAATGG  CAGGCAGGAA  AGACAGAGGA

481  AGGAAGGAGG  GAGAAGGGAA  GGAGTGAAGG  AAGGAGTGAA  AAAGGTAAGG  AAGAAAGGGA

541  ATAGGGGAGG  AAGGGAGGAA  ATGGGAAGGG  AAAGAAGGAA  AGGAAGGAAA  GAGGGAGGGA

601  AGAAAGGAAG  GGAAAAGGGA  GGGAGTGAGT  GAATGAAAGA  TGGAAAGAAG  GAAGAAAGGG

661  AGGGAGGCAG  GGAGGAAAGA  AAGTTGCGCT  TCCCTTGAGC  TGCCATGGGC  ACTGACTCTT

721  AGGGTCTGAA  AGCCCCTGAG  ATGCAAAAGC  CTAGTGCTCA  CAAAGAGCTG  GAAAGCCTCA

781  AGGAAGTTCT  TCAATATTTT  TGGAAGGAAA  CTGTCTCCAG  AAGCTTCCCT  CCCACGACA

841  GATAATGAGC  AGCAAGTGCT  TCTGGCGACT  TAGGGTGATG  TGAAATCACG  CTGGGAATCC

901  TGCTCCTCCT  CAGGTCCTGG  CAGTTTCAGG  GCCCCTCCCT  AGGCCTTACT  TAAAAGGCTG

961  AGGCATCCTT  GGAGGAACAG  GCAGACTCCA  CAGCTCCCGC  CAGGAGAAAG  GAACATTCTG

1021  AGGTATGCTC  TGGGGCGCTG  GTGGTACCGG  AGCTCTCTCC  TGACCCCAGA  CCCAGAATCT

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1081 GCTCCGTGGA GGCTGTTTAC ATGCTGGGGA GCTCGGTGCA GCTGCTTGCT CCCCAGACCC
1141 CAGCCAACTC AGCCTCTCTC TCCATGATTT TCTGTTGTTT ATTCCAAAAT AGGGGAGTCT
1201 ACACCCTGTG GAGCTCAAGA TGGTCCTGAG TGGGGCGCTG TGCTTCCGGT GAGTGTATGA
1261 GGCCCTGGTT TGGTGGTGTC CTCCGGAGGA AGTGAGTTCT GGATAGACCC GTTGTCCAGC
1321 TCTGAGCAGG AGGGAGGAAG GGAGGGGCTG CCATTGCAGC TGGGAAATTG TGACCAGCAC
1381 CTCATTGCTC TTAGAGTTTT CCCAGCCTTT TTCAAATAGG GGCAGGACTG GGGCAGGCCA
1441 TCTCACAAGG GGTCCCTGAT GCTGAGGGGG ACAAGTGAAC CTCCCAGTCT AGAGCTCCAG
1501 CCAAGTCTAT CCAAGGTGGG AACGGGGGCC AGGATCCCTG CTCAGAGCTC CGCCATTGTC
1561 CCCCATCACA GTGAATGGAT GTAAGCTCAC CCACTCTGTG CCCCTACCTC CCTGCTACTC
1621 TTTGGGGATA ATAATAAAC AAAAACCATT ACCATCAGCC AGTCTGTCCA CCCACTGGCA
1681 TGTACCAAGC CAGACACTCT GCCGTGTTCT GGGCTTAACA ACAGAGGATG AGAGTGGTCC
1741 TTTCTCTCAG TCTAATAAAG CACTTCCCAC GATGTGTTCT ATGGGACTCG ATTAGAGGAG
1801 TCCCACAGAG GCATCCAGGA GATGCTTTAC ACAGTGGAGC TCTCTGATCA AGTAAATGCA
1861 GGGAATTCTG CTTTCTACAT CCTCTCATAA GAGAACCACA GCCCAGCTCA GCATATGAGT
1921 GACTGAGGTT TTCTGAAGTA AGGCAACTTG TTGAATCGTA TTTAGCTATG CATCGACCCA
1981 ATTTTACAC TGCATCCTTT TCCCCATAT AACTTTTGGA GAAACCCACT TTAGGATACA
2041 TCTTCCACCT CATAGGATGC CAGGAAATCA ACTGAGTTCA AAGATGAGAA ACAACTTTGA
2101 AAAGTTAAAT AAAAGAAATT TAAATTTAAA GAAACTCCTC ACTTAGTAAG GAATATATGA
2161 CCAAATAGAA ATACATGTAT CTTGAAGAAT TGAAGAATCA GGCTTTAACG TGGAAGAGGC

2221 CTGGATGTTA TCCAACCCAT CATCTTAGTG TAGCAATGGG GAGGCTCAGG CCCAGAGTGG
2281 GCGAGAGAGT TGTCTCCTGC GACTCAGCAG CATTGGAGGC ATAGATGGGG CAAGAACCTA
2341 GGGCTCTGAC TCACCGTGCA GCTTCTCTTC CAACAGGAGA TGGGTTGGGG CAGAAAAGGT
2401 TGAATAGGGT GAAGGAGCAA ACCACAGACT CCAGTGGGAG ACTGTGGGGT CATCCTCCTT
2461 GTAGGGCATG AGCCCAGCAG GGCTGGGAGA CAAGGCTGTG CTGTTACTTC TGGCACAGTA
2521 GGAAGAAAGA GAGACAAAAT GCCTGAGATC AGGGGGTTCT CTGGATCCAG GGCATGCTGG
2581 AGTGTCACC CTCCTCCTAA TGTAGTCCTC ACCCCTTCCT GATGTTTCAG AATGAAGGAC
2641 TCGGCATTGA AGGTGCTTTA TCTGCATAAT AACCAGCTTC TAGCTGGAGG GCTGCATGCA
2701 GGAAGGTCA TTAAAGGTG GTGATGAAAC ATGACCCACT TTCCTTGGTC TCTATACT
2761 CTCAGGGGAG GGGGCCTGAA GAGGGCTTAG AATAGTCATA CAGATTAGCA TAGGCCTACA
2821 GAGCCCAGGC ATTAGGGCAG CACAAACCAG GCTCTAAGCA AAGGCAAATA AAATACTACA
2881 CCTCTCAGCA AAGTGAAGAC ACACGCTCTG GGGCCACCTG AAGCTTCTGT GCAGAAGTGA
2941 GAATGTTTTT CAAGAGGCTT GTCTTGTCAT TCCCTTACAG GTAGATTTAG GTCAAGCATT
3001 GCATTCCCTG GGAGCCAGTA AGTACCAAGG AGAGAACTAA CGTAGATTCT CTATACCTTT
3061 TTTCCCATAT GGGAGTGGGT TTCTGCCTCT CCACCCTGGG TCCCCTCTGC TCTCTGAAGA
3121 TCCTCAGTCA CTTAGAGTGG AGGGACCCAG AGAACAGGTG GCATTGTTGG ACCTCCTGCT
3181 TGCTCACTCT GCCCCATGCA CTGCAACAGG TCCCTCTCTA AAATAGTTTG CACCTGCCCCA
3241 CCTGGGGCAC CTTGCTGAG CACAGATGCC AGGTAGATCC TTCAGCTAGG CCATATGTGT
3301 ATGTGTGTGC TTA CTGGTGT ATGTATGTGT GCATGCAGGC ATATATGTGT GAGCATATGT

3361 GTGCATGCAT GTATCTGTAT GTAACCATGT ATGTGTGAGT GCAGGTATGT AGGTATGAGC
3421 ATGTGTGTGT ATATGTATAT GTGTGCATGC ATGTATCTGT GCATGTATGT ATCTGATGTA
3481 TGTGGGTGGT GAGGGGATGT ACAGAGAGGA ATGAGACCCT CTTTGTCTCT CAGCAACCTC
3541 ACAGGGTGTA GAAAGTTGTC CAAACAATTC CAAAGGGGGG CTTATTAAGA CAGGGTTCAG
3601 AAAAAGGCCCT GAGACCCAAG GGGCATTAAA GGAGGGGGTT GAGTCTATTT TGGGTGTAG
3661 AGGCTTGAAG ATTTGACCCT GAACTAGAGG GTGGAGTGGA GGTGGTACAA TGTGCTTCCA
3721 TGCCTTGATG TCCACTCTGG GCCAGTGGAC AGGAGAAGCC ATGTCATGAC AGCTGCTGAG
3781 AAGCCTCCCT TCTGCCCAGC CTGGGGGCAG GCCGTCTCAC AGCAGTCCTG TGCCCTAGAG
3841 CCCAGGACAG GGAAGAAGG AGGGAAAGGC ATCCAGGGCC CTGCATCTGG CCTCTTTCCC
3901 ACAGGTGAAG AGATCAGCGT GGTCCCCAAT CGGTGGCTGG ATGCCAGCCT GTCCCCCGTC
3961 ATCCTGGGTG TCCAGGGTGG AAGCCAGTGC CTGTCATGTG GGGTGGGGCA GGAGCCGACT
4021 CTAACACTAG AGGTGAGACT TGGGGCATCC TCACTGGGGA CTCAGCCACA GATGCTGAGC
4081 CTACTIONAAGC CGGGCAGCCC ACAGCCCTGG TGCTGTGGGA CACCCTAGCA GGATTCTGTT
4141 GATGGCAGCT TTGCCTCCTC CCTAAGGATC CTGCCCAGCC CTCCCTCTGC CCCTGCTTCT
4201 GCCCTCACCT GACCTCCCCT CCTCTGCCGG CAGCCAGTGA ACATCATGGA GCTCTATCTT
4261 GGTGCCAAGG AATCCAAGAG CTTACCTTC TACCGGCGGG ACATGGGGCT CACCTCCAGC
4321 TTCGAGTCGG CTGCCTACCC GGGCTGGTTC CTGTGCACGG TGCCTGAAGC CGATCAGCCT
4381 GTCAGACTCA CCCAGCTTCC CGAGAATGGT GGCTGGAATG CCCCATCAC AGACTTCTAC
4441 TTCCAGCAGT GTGACTAGGG CAACGTGCCC CCCAGAACTC CCTGGGCAGA GCCAGCTCGG

4501 GTGAGGGGTG AGTGGAGGAG ACCCATGGCG GACAATCACT CTCTCTGCTC TCAGGACCCC
4561 CACGTCTGAC TTAGTGGGCA CCTGACCACT TTGTCTTCTG GTTCCCAGTT TGGATAAATT
4621 CTGAGATTTG GAGCTCAGTC CACGGTCCTC CCCCCTGGA TGGTGCTACT GCTGTGGAAC
4681 CTTGTAAAAA CCATGTGGGG TAAACTGGGA ATAACATGAA AAGATTTCTG TGGGGGTGGG
4741 GTGGGGGAGT GGTGGGAATC ATTCCTGCTT AATGGTAACT GACAAGTGTT ACCCTGAGCC
4801 CCGCAGGCCA ACCCATCCCC AGTTGAGCCT TATAGGGTCA GTAGCTCTCC ACATGAAGTC
4861 CTGTCACTCA CCACTGTGCA GGAGAGGGAG GTGGTCATAG AGTCAGGGAT CTATGGCCCT
4921 TGGCCCAGCC CCACCCCTT CCCTTTAATC CTGCCACTGT CATATGCTAC CTTTCCTATC
4981 TCTTCCCTCA TCATCTTGTT GTGGGCATGA GGAGGTGGTG ATGTCAGAAG AAATGGCTCG
5041 AGCTCAGAAG ATAAAAGATA AGTAGGGTAT GCTGATCCTC TTTTAAAAAC CCAAGATACA
5101 ATCAAAATCC CAGATGCTGG TCTCTATTCC CATGAAAAG TGCTCATGAC ATATTGAGAA
5161 GACCTACTTA CAAAGTGGCA TATATTGCAA TTTATTTTAA TTAAAAGATA CCTATTTATA
5221 TATTTCTTTA TAGAAAAAAG TCTGGAAGAG TTTACTTCAA TTGTAGCAAT GTCAGGGTGG
5281 TGGCAGTATA GGTGATTTTT CTTTAAATTC TGTTAATTTA TCTGTATTTT CTAATTTTTT
5341 TACAATGAAG ATGAATTCCT TGTATAAAAA TAAGAAAAGA AATTAATCTT GAGGTAAGCA
5401 GAGCAGACAT CATCTCTGAT TGTCTCAGC CTCCACTTCC CCAGAGTAAA TTCAAATTGA
5461 ATCGAGCTCT GCTGCTCTGG TTGGTTGTAG TAGTGATCAG GAAACAGATC TCAGCAAAGC
5521 CACTGAGGAG GAGGCTGTGA TGAGTTTGTG TGGCTGGAAT CTCTGGGTAA GGAACTTAAA
5581 GAACAAAAAT CATCTGGTAA TTCTTTCCTA GAAGGATCAC AGCCCCTGGG ATTCCAAGGC

5641 ATTGGATCCA GTCTCTAAGA AGGCTGCTGT ACTGGTTGAA TTGTGTCCCC CTCAAATTCA
5701 CATCCTTCTT GGAATCTCAG TCTGTGAGTT TATTTGGAGA TAAGGTCTCT GCAGATGTAG
5761 TTAGTTAAGA CAAGGTCATG CTGGATGAAG GTAGACCTAA ATTCAATATG ACTGGTTTCC
5821 TTGTATGAAA AGGAGAGGAC ACAGAGACAG AGGAGACGCG GGAAGACTA TGTAAGATG
5881 AAGGCAGAGA TCGGAGTTTT GCAGCCACAA GCTAAGAAAC ACCAAGGATT GTGGCAACCA
5941 TCAGAAGCTT GGAAGAGGCA AAGAAGAATT CTTCCCTAGA GGCTTTAGAG GGATAACGGC
6001 TCTGCTGAAA CCTTAATCTC AGACTTCCAG CTCCTGAAC GAAGAAAGAA TAAATTTCCG
6061 CTGTTTTAAG CCACCAAGGA TAATTGGTTA TGGCAGCTCT AGGAAACTAA TACAGCTGCT
6121 AAAATGATCC CTGTCTCCTC GTGTTTACAT TCTGTGTGTG TCCCCTCCCA CAATGTACCA
6181 AAGTTGTCTT TGTGACCAAT AGAATATGGC AGAAGTGATG GCATGCCACT TCCAAGATTA
6241 GGTTATAAAA GACACTGCAG CTTCTACTTG AGCCCTCTCT CTCTGCCACC CACCGCCCCC
6301 AATCTATCTT GGCTCACTCG CTCTGGGGGA AGCTAGCTTC CATGCTATGA GCAGGCCTAT
6361 AAAGAGACTT ATGTGGTAAA AAATGAAGTC TCCTGCCCAC AGCCACATTA GTGAACCTAG
6421 AAGCAGAGAC TCTGTGAGAT AATCAATGTT TGTTGTTTTA AGTTGCTCAG TTTTGGTCTA
6481 ACTTGTTATG CAGCAATAGA TAAATAATAT GCAGAGAAAG AGAAACAAAT GCATTTGTTT

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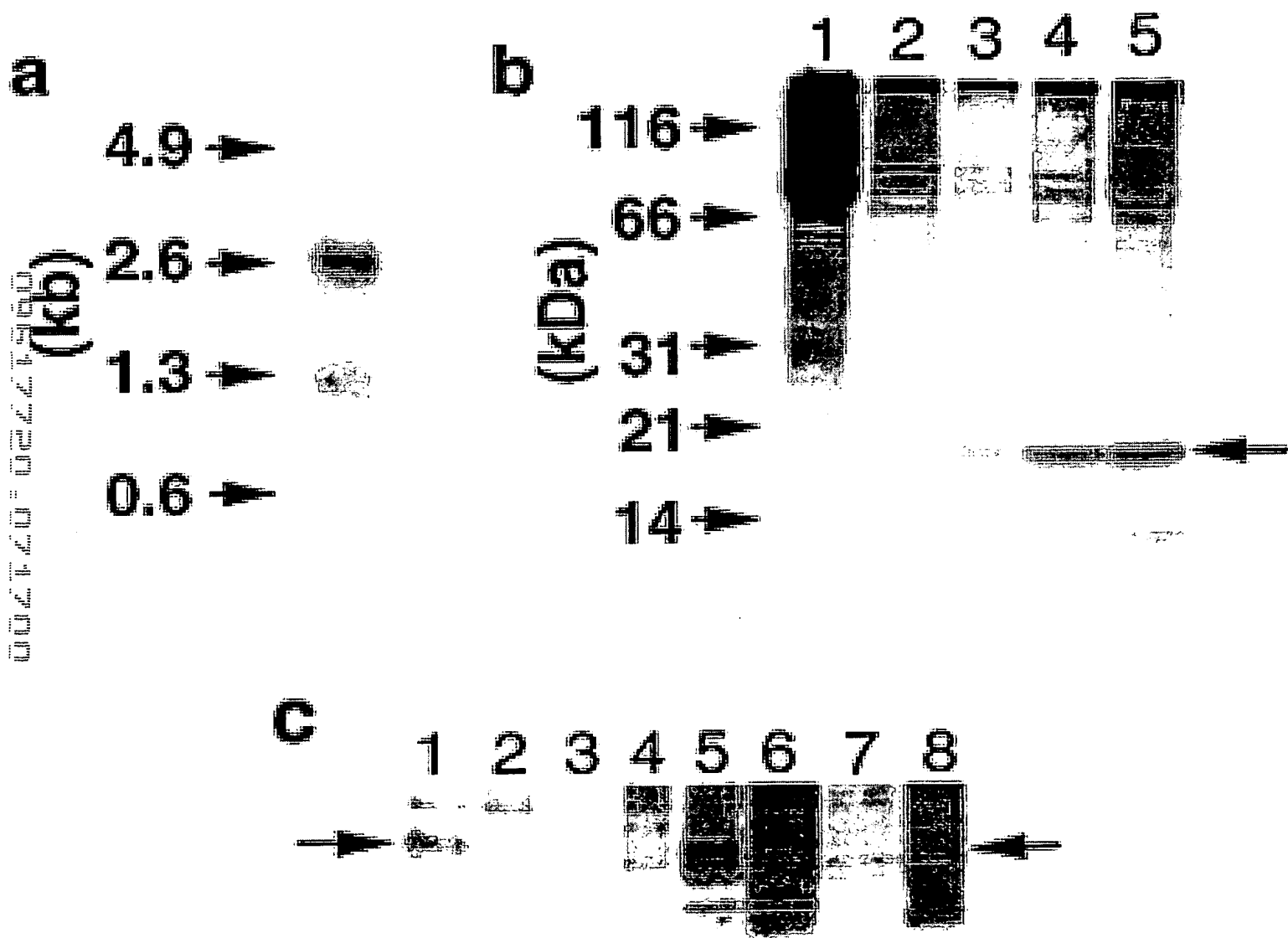


FIG. 12

	Sheet 1	Sheet 2	Sheet 3	Sheet 4
	* * * * *	**	***	* * *
	>>>>>>>>	>>>>>	>>>>>	>>>>>>>>
h1L-1L1		MVLSGALCFRMRKDSALKVLYLH	NNQLLAG	GLHAGKVLKGEISVVP
m1L-1L1		MVLSGALCFRMRKDSALKVLYLH	NNQLLAG	GLHAEKVIKGEISVVP
h1L-1ra	RPSGRKSSKMQAERIMDVNQKTFYLR	NNQLVAG	YLGQPNVNLKIDVVP	
h1L-1beta	APVRSINCTLRDSQOKSLVMSGPEYELKAL	HLQGDMEQVVFMSMF		
h1L-1alpha	SAPFSFLSNVKYNFMRIKYEFIINDALNQSIIRANDQYLTAAALHNLD EAV KFDMGAY			
h1L-18	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAP	RTIFLISMY		

	Sheet 5	Sheet 6	Sheet 7	Sheet 8
	* * * * *	* * * * *	*****	**
	>>>>>	>>>>>>>	>>>>>>>>	>>>>>
h1L-1L1	NRWLDASLSPVILGVQG	GSQCLSCG	VGEQPTLTLEPVNIMELYLGAKESKSTFYRR	
m1L-1L1	NRA LDASLSPVILGVQG	GSQCLSCG	TEKGPI LKLEPVNIMELYLGAKESKSTFYRR	
h1L-1ra	IEPHALFLGIHG	GKMCISCVKS	DETRIQLEAVNITDLS ENRKQDKRFAPFIRS	
h1L-1beta	VQGEESNDKIPVALGLK	EKNLYLSCVLKDKPTIQLESVDPKNYPK	KKMEKREVENKI	
h1L-1alpha	KSSKDPDAKITVILRIS	KTQLYVTAQ	DEDQPVLLKEMPEIPKTIIT	GSETNLLFWE
h1L-18	KDSQ PRGMVITISVKCEKISTLSCE	NKII SFKEMNPDPNIXDKTSDIIF	QORSVP	

	Sheet 9	Sheet 10	Sheet 11	Sheet 12
	* * * * *	* * * * *	*****	* * * * *
	>>>>>>>>	>>>>>>>	>>>>>>>>	>>>>>>>>
h1L-1L1	DMGLTSSFESAYPGWFLCTV	PEADQPVRLTQLP	PENGGWNNAPITDFYFQQCD	
m1L-1L1	DMGLTSSFESAYPGWFLCTV	PEADQPVRLTQLP	EDPAWDAPITDFYFQQCD	
h1L-1ra	DSGPTTSFESAACPWFELCTA	MEADQVSLTNMPDEG	VMVTKFYFQDEDE	
h1L-1beta	EINNKLFEESAQFPNWIIST	QAENMPVFLGTTKGQ	DITDFTMQFVSS	
h1L-1alpha	THGTKNYFTISVAHPNLFIAT	KQDYWVCLAGGP	P	SITDFQILENQA
h1L-18	GHDNKMQFESSSYEGYFLACEKERDL	FKLILKKEDELG	DRSIMETVQNEED	